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* * * * * Welcome to STN International * * * * *

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NEWS 3 DEC 05 CASREACT(R) - Over 10 million reactions available
NEWS 4 DEC 14 2006 MeSH terms loaded in MEDLINE/LMEDLINE
NEWS 5 DEC 14 2006 MeSH terms loaded for MEDLINE file segment of TOXCENTER
NEWS 6 DEC 14 CA/CAPLUS to be enhanced with updated IPC codes
NEWS 7 DEC 21 IPC search and display fields enhanced in CA/CAPLUS with the
IPC reform
NEWS 8 DEC 23 New IPC8 SEARCH, DISPLAY, and SELECT fields in USPATFULL/
USPAT2
NEWS 9 JAN 13 IPC 8 searching in IFIPAT, IFIUIDB, and IFICDB
NEWS 10 JAN 13 New IPC 8 SEARCH, DISPLAY, and SELECT enhancements added to
INPADOC
NEWS 11 JAN 17 Pre-1988 INPI data added to MARPAT
NEWS 12 JAN 17 IPC 8 in the WPI family of databases including WPIFV
NEWS 13 JAN 30 Saved answer limit increased
NEWS 14 JAN 31 Monthly current-awareness alert (SDI) frequency
added to TULSA

NEWS EXPRESS JANUARY 03 CURRENT VERSION FOR WINDOWS IS V8.01,
CURRENT MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP),
AND CURRENT DISCOVER FILE IS DATED 19 DECEMBER 2005.
V8.0 USERS CAN OBTAIN THE UPGRADE TO V8.01 AT
<http://download.cas.org/express/v8.0-Discover/>

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of commercial gateways or other similar uses is prohibited and may
result in loss of user privileges and other penalties.

* * * * * STN Columbus * * * * *

FILE 'HOME' ENTERED AT 17:18:39 ON 09 FEB 2006

=> FIL CAPLUS

| COST IN U.S. DOLLARS | SINCE FILE ENTRY | TOTAL SESSION |
|----------------------|---------------------|------------------|
| FULL ESTIMATED COST | 0.21 | 0.21 |

FILE 'CAPLUS' ENTERED AT 17:18:49 ON 09 FEB 2006

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FILE COVERS 1907 - 9 Feb 2006 VOL 144 ISS 7
FILE LAST UPDATED: 8 Feb 2006 (20060208/ED)

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=> s tgtagcggcccacgctgg/sqsn

REGISTRY INITIATED

Substance data SEARCH and crossover from CAS REGISTRY in progress...
Use DISPLAY HITSTR (or FHITSTR) to directly view retrieved structures.

L2 0 L1

=> s taccacgcgacacacttc/sqsn

REGISTRY INITIATED

Substance data SEARCH and crossover from CAS REGISTRY in progress...
Use DISPLAY HITSTR (or FHITSTR) to directly view retrieved structures.

L4 1 L3

=> d 14

L4 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2006 ACS on STN

AN 2002:10074 CAPLUS

DN 136:65204

TI Transgenic corn plant PV-ZMGT32 (nk603) transformed with DNA construct containing 5-enolpyruvylshikimate 3-phosphate synthase for conferring glyphosate tolerance

IN Behr, Carl F.; Hironaka, Catherine; Heck, Gregory R.; You, Jinsong

PA Monsanto Technology Llc, USA

SO Eur. Pat. Appl., 25 pp.

CODEN: EPXXDW

DT Patent

LA English

FAN.CNT 1

| | PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|----|---|------|----------|-----------------|----------|
| PI | EP 1167531 | A1 | 20020102 | EP 2001-202314 | 20010615 |
| | R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO | | | | |
| | BR 2001000752 | A | 20020213 | BR 2001-752 | 20010222 |
| | ZA 2001004092 | A | 20011119 | ZA 2001-4092 | 20010518 |
| | US 2002013960 | A1 | 20020131 | US 2001-872051 | 20010601 |

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US 6825400      B2      20041130
EP 1582592      A1      20051005      EP 2005-105879      20010615
R:  AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
    IE, SI, LT, LV, FI, RO, MK, CY, AL, TR
CA 2349841      AA      20011222      CA 2001-2349841      20010620
CN 1332246      A       20020123      CN 2001-122036      20010622
BG 105637       A       20020430      BG 2001-105637      20010622
US 2004139493   A1      20040715      US 2004-790430      20040301
PRAI US 2000-213567P   P       20000622
US 2000-240014P   P       20001013
US 2000-241215P   P       20001013
US 2001-872051   A3      20010601
EP 2001-202314   A3      20010615
RE.CNT 3      THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD
                ALL CITATIONS AVAILABLE IN THE RE FORMAT

```

=> s accaagcttttataatag/sqsn

REGISTRY INITIATED

Substance data SEARCH and crossover from CAS REGISTRY in progress...
 Use DISPLAY HITSTR (or FHITSTR) to directly view retrieved structures.

L6 1 L5

=> d 16

```

L6 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2002:10074 CAPLUS
DN 136:65204
TI Transgenic corn plant PV-ZMGT32 (nk603) transformed with DNA construct
    containing 5-enolpyruvoylshikimate 3-phosphate synthase for conferring
    glyphosate tolerance
IN Behr, Carl F.; Hironaka, Catherine; Heck, Gregory R.; You, Jinsong
PA Monsanto Technology Llc, USA
SO Eur. Pat. Appl., 25 pp.
    CODEN: EPXXDW
DT Patent
LA English
FAN.CNT 1
PATENT NO.      KIND      DATE      APPLICATION NO.      DATE
-----
PI EP 1167531    A1      20020102    EP 2001-202314      20010615
R:  AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
    IE, SI, LT, LV, FI, RO
BR 2001000752    A       20020213    BR 2001-752          20010222
ZA 2001004092    A       20011119    ZA 2001-4092          20010518
US 2002013960    A1      20020131    US 2001-872051      20010601
US 6825400      B2      20041130
EP 1582592      A1      20051005    EP 2005-105879      20010615
R:  AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
    IE, SI, LT, LV, FI, RO, MK, CY, AL, TR
CA 2349841      AA      20011222    CA 2001-2349841      20010620
CN 1332246      A       20020123    CN 2001-122036      20010622
BG 105637       A       20020430    BG 2001-105637      20010622
US 2004139493   A1      20040715    US 2004-790430      20040301
PRAI US 2000-213567P   P       20000622
US 2000-240014P   P       20001013
US 2000-241215P   P       20001013
US 2001-872051   A3      20010601
EP 2001-202314   A3      20010615
RE.CNT 3      THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD
                ALL CITATIONS AVAILABLE IN THE RE FORMAT

```

=> d his

(FILE 'HOME' ENTERED AT 17:18:39 ON 09 FEB 2006)

FILE 'CAPLUS' ENTERED AT 17:18:49 ON 09 FEB 2006
S TGTAGCGGCCACGCTGG/SQSN

L1 FILE 'REGISTRY' ENTERED AT 17:19:17 ON 09 FEB 2006
0 S TGTAGCGGCCACGCTGG/SQSN

L2 FILE 'CAPLUS' ENTERED AT 17:19:37 ON 09 FEB 2006
0 S L1
S TACCACGCGACACACTTC/SQSN

L3 FILE 'REGISTRY' ENTERED AT 17:20:40 ON 09 FEB 2006
6 S TACCACGCGACACACTTC/SQSN

L4 FILE 'CAPLUS' ENTERED AT 17:21:00 ON 09 FEB 2006
1 S L3
S ACCAAGCTTTTATAATAG/SQSN

L5 FILE 'REGISTRY' ENTERED AT 17:22:13 ON 09 FEB 2006
8 S ACCAAGCTTTTATAATAG/SQSN

L6 FILE 'CAPLUS' ENTERED AT 17:22:35 ON 09 FEB 2006
1 S L5



results of **BLAST**

BLASTN 2.2.13 [Nov-27-2005]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

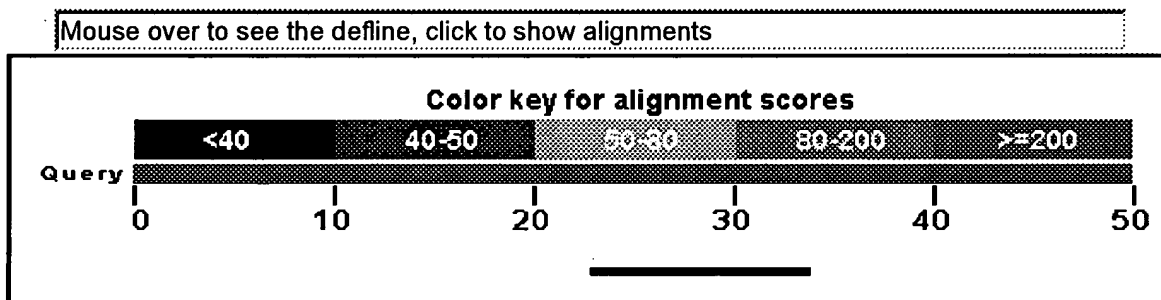
RID: 1139520495-2564-183997461739.BLASTQ4

Database: NCBI Genomic Reference Sequences
648,380 sequences; 5,833,944,919 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)
[Taxonomy reports](#)

Query=
Length=50

Distribution of 2 Blast Hits on the Query Sequence



| Sequences producing significant alignments: | Score (Bits) | E Value |
|--|-----------------|------------|
| gi 11994090 ref NC_001666.2 Zea mays chloroplast, complete geno | 22.3 | 1.1 |

Alignments

Get selected sequences

Select all

Deselect all

> [gi|11994090|ref|NC_001666.2|](#) [Zea mays chloroplast, complete genome](#)
Length=140384

Score = 22.3 bits (11), Expect = 1.1
Identities = 11/11 (100%), Gaps = 0/11 (0%)
Strand=Plus/Plus

Query 24 AGGGTGAAGTA 34
|||||||
Sbjct 96767 AGGGTGAAGTA 96777

Score = 22.3 bits (11), Expect = 1.1
Identities = 11/11 (100%), Gaps = 0/11 (0%)
Strand=Plus/Minus

Query 24 AGGGTGAAGTA 34
|||||||
Sbjct 125970 AGGGTGAAGTA 125960

Database: NCBI Genomic Reference Sequences
Posted date: Feb 7, 2006 12:38 PM
Number of letters in database: 142,297
Number of sequences in database: 2
Lambda K H
1.37 0.711 1.31
Gapped
Lambda K H
1.37 0.711 1.31
Matrix: blastn matrix:1 -3
Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 2
Number of Hits to DB: 0
Number of extensions: 0
Number of successful extensions: 0
Number of sequences better than 10: 0
Number of HSP's better than 10 without gapping: 0
Number of HSP's gapped: 0
Number of HSP's successfully gapped: 0
Length of query: 50
Length of database: 142297
Length adjustment: 11
Effective length of query: 39
Effective length of database: 142297
Effective search space: 5549583
Effective search space used: 5548725
A: 0
X1: 10 (19.8 bits)
X2: 15 (29.7 bits)
X3: 25 (49.6 bits)
S1: 10 (20.3 bits)
S2: 10 (20.3 bits)



results of **BLAST**

BLASTN 2.2.13 [Nov-27-2005]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

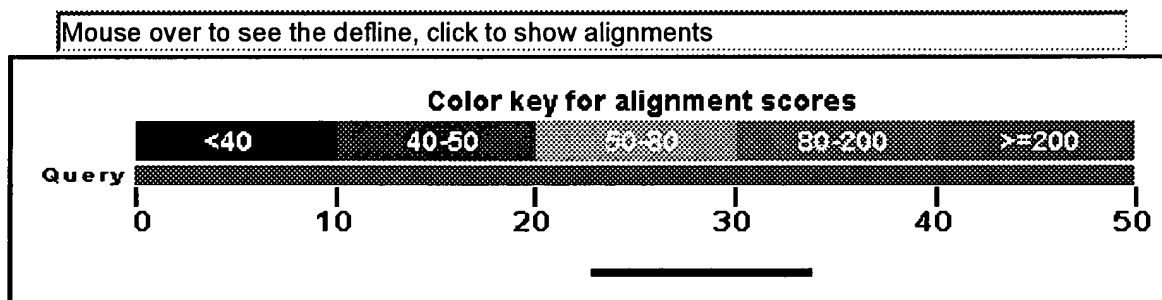
RID: 1139520495-2564-183997461739.BLASTQ4

Database: NCBI Genomic Reference Sequences
648,380 sequences; 5,833,944,919 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)
[Taxonomy reports](#)

Query=
Length=50

Distribution of 2 Blast Hits on the Query Sequence



| Sequences producing significant alignments: | Score (Bits) | E Value |
|--|----------------------|---------------------|
| gi 11994090 ref NC_001666.2 Zea mays chloroplast, complete geno | 22.3 | 1.1 |

Alignments

Get selected sequences

Select all

Deselect all

> [gi|11994090|ref|NC_001666.2|](#) [Zea mays chloroplast, complete genome](#)
Length=140384

Score = 22.3 bits (11), Expect = 1.1
Identities = 11/11 (100%), Gaps = 0/11 (0%)
Strand=Plus/Plus

Query 24 AGGGTGAAGTA 34
|||||||
Sbjct 96767 AGGGTGAAGTA 96777

Score = 22.3 bits (11), Expect = 1.1
Identities = 11/11 (100%), Gaps = 0/11 (0%)
Strand=Plus/Minus

Query 24 AGGGTGAAGTA 34
|||||||
Sbjct 125970 AGGGTGAAGTA 125960

Database: NCBI Genomic Reference Sequences
Posted date: Feb 7, 2006 12:38 PM
Number of letters in database: 142,297
Number of sequences in database: 2
Lambda K H
1.37 0.711 1.31
Gapped
Lambda K H
1.37 0.711 1.31
Matrix: blastn matrix:1 -3
Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 2
Number of Hits to DB: 0
Number of extensions: 0
Number of successful extensions: 0
Number of sequences better than 10: 0
Number of HSP's better than 10 without gapping: 0
Number of HSP's gapped: 0
Number of HSP's successfully gapped: 0
Length of query: 50
Length of database: 142297
Length adjustment: 11
Effective length of query: 39
Effective length of database: 142297
Effective search space: 5549583
Effective search space used: 5548725
A: 0
X1: 10 (19.8 bits)
X2: 15 (29.7 bits)
X3: 25 (49.6 bits)
S1: 10 (20.3 bits)
S2: 10 (20.3 bits)



results of **BLAST**

BLASTN 2.2.13 [Nov-27-2005]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1139520711-10093-27750649669.BLASTQ4

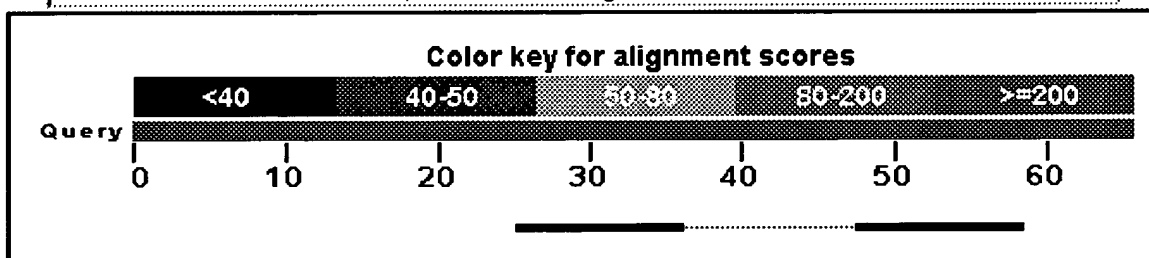
Database: NCBI Genomic Reference Sequences
648,380 sequences; 5,833,944,919 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)
[Taxonomy reports](#)

Query=
Length=65

Distribution of 3 Blast Hits on the Query Sequence

Mouse over to see the define, click to show alignments



| Sequences producing significant alignments: | Score (Bits) | E Value |
|--|----------------------|------------|
| gi 11994090 ref NC_001666.2 Zea mays chloroplast, complete geno | 22.3 | 1.5 |

Alignments

Get selected sequences

Select all

Deselect all

> ☐ [gi|11994090|ref|NC_001666.2|](#) ☒ Zea mays chloroplast, complete genome
Length=140384

Score = 22.3 bits (11), Expect = 1.5
Identities = 11/11 (100%), Gaps = 0/11 (0%)
Strand=Plus/Plus

Query 48 GATCTTTTCTC 58
 |||||
 Sbjct 44568 GATCTTTTCTC 44578

Score = 22.3 bits (11), Expect = 1.5
 Identities = 11/11 (100%), Gaps = 0/11 (0%)
 Strand=Plus/Plus

Query 26 TCCTCCTCTCT 36
 |||||
 Sbjct 83760 TCCTCCTCTCT 83770

Score = 22.3 bits (11), Expect = 1.5
 Identities = 11/11 (100%), Gaps = 0/11 (0%)
 Strand=Plus/Minus

Query 26 TCCTCCTCTCT 36
 |||||
 Sbjct 138977 TCCTCCTCTCT 138967

Database: NCBI Genomic Reference Sequences
 Posted date: Feb 7, 2006 12:38 PM
 Number of letters in database: 142,297
 Number of sequences in database: 2
 Lambda K H
 1.37 0.711 1.31
 Gapped
 Lambda K H
 1.37 0.711 1.31
 Matrix: blastn matrix:1 -3
 Gap Penalties: Existence: 5, Extension: 2
 Number of Sequences: 2
 Number of Hits to DB: 0
 Number of extensions: 0
 Number of successful extensions: 0
 Number of sequences better than 10: 0
 Number of HSP's better than 10 without gapping: 0
 Number of HSP's gapped: 0
 Number of HSP's successfully gapped: 0
 Length of query: 65
 Length of database: 142297
 Length adjustment: 11
 Effective length of query: 54
 Effective length of database: 142297
 Effective search space: 7684038
 Effective search space used: 7682850
 A: 0
 X1: 10 (19.8 bits)
 X2: 15 (29.7 bits)
 X3: 25 (49.6 bits)
 S1: 10 (20.3 bits)



results of BLAST

BLASTN 2.2.13 [Nov-27-2005]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

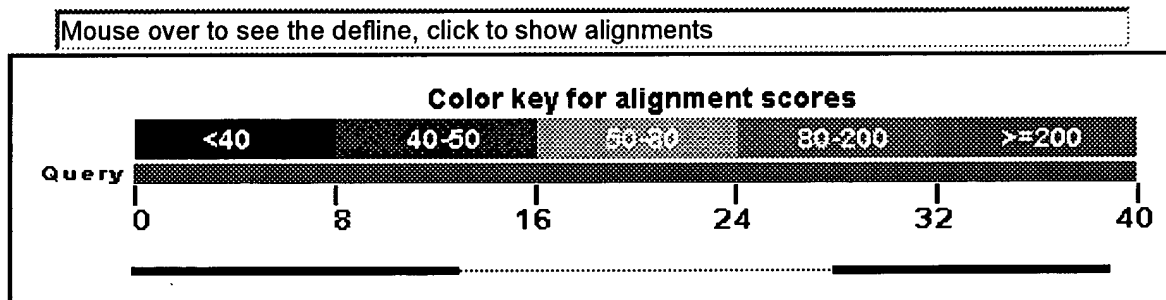
RID: 1139520074-12515-142933253334.BLASTQ4

Database: NCBI Genomic Reference Sequences
648,380 sequences; 5,833,944,919 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)
[Taxonomy reports](#)

Query=
Length=40

Distribution of 3 Blast Hits on the Query Sequence



| Sequences producing significant alignments: | | Score (Bits) | E Value |
|---|-------------------------------------|-----------------|------------|
| gi 11994090 ref NC_001666.2 | Zea mays chloroplast, complete geno | 22.3 | 0.80 |

Alignments

Get selected sequences Select all Deselect all

> ☒ gi|11994090|ref|NC_001666.2| ☒ Zea mays chloroplast, complete genome
Length=140384

Score = 22.3 bits (11), Expect = 0.80
Identities = 11/11 (100%), Gaps = 0/11 (0%)
Strand=Plus/Plus

Query 3 TCGATCCAAAA 13
 |||||
 Sbjct 66973 TCGATCCAAAA 66983

Score = 22.3 bits (11), Expect = 0.80
 Identities = 11/11 (100%), Gaps = 0/11 (0%)
 Strand=Plus/Plus

Query 1 AATCGATCCAA 11
 |||||
 Sbjct 73754 AATCGATCCAA 73764

Score = 22.3 bits (11), Expect = 0.80
 Identities = 11/11 (100%), Gaps = 0/11 (0%)
 Strand=Plus/Plus

Query 29 TGGAAGAAAGA 39
 |||||
 Sbjct 112529 TGGAAGAAAGA 112539

Database: NCBI Genomic Reference Sequences

Posted date: Feb 7, 2006 12:38 PM

Number of letters in database: 142,297

Number of sequences in database: 2

Lambda K H
 1.37 0.711 1.31

Gapped

Lambda K H
 1.37 0.711 1.31

Matrix: blastn matrix:1 -3

Gap Penalties: Existence: 5, Extension: 2

Number of Sequences: 2

Number of Hits to DB: 0

Number of extensions: 0

Number of successful extensions: 0

Number of sequences better than 10: 0

Number of HSP's better than 10 without gapping: 0

Number of HSP's gapped: 0

Number of HSP's successfully gapped: 0

Length of query: 40

Length of database: 142297

Length adjustment: 11

Effective length of query: 29

Effective length of database: 142297

Effective search space: 4126613

Effective search space used: 4125975

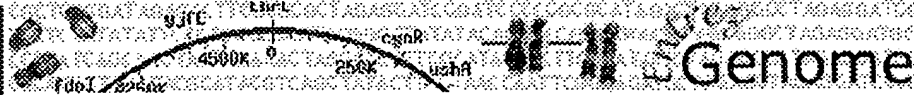

A: 0

X1: 10 (19.8 bits)

X2: 15 (29.7 bits)

X3: 25 (49.6 bits)

S1: 10 (20.3 bits)




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All: 1 

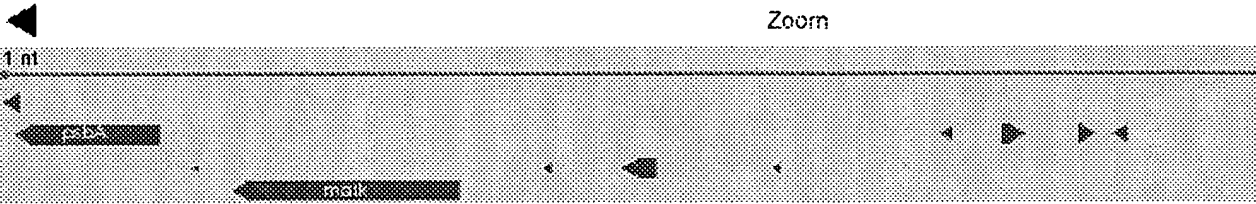
Genome > Eukaryota > Zea mays chloroplast, complete genome

Lineage: [Eukaryota](#) ; [Viridiplantae](#) ; [Streptophyta](#) ; [Streptophytina](#) ; [Embryophyta](#) ; [Tracheophyta](#) ; [Euph Magnoliophyta](#) ; [Liliopsida](#) ; [commelinids](#) ; [Poales](#) ; [Poaceae](#) ; [PACCAD clade](#) ; [Panicoideae](#) ; [Andropog](#)

| Genome Info: | Feature table: | BLAST homologs: | Links: | Review |
|-----------------------------------|-------------------------------------|-----------------|--------------------------------|---------------------------|
| Refseq: NC_001666 | Proteins: 111 | COG | Genome Project | Public |
| GenBank: X86563 | Structural RNAs: 47 | 3D Structure | Refseq FTP | Refse |
| Length: 140,384 nt | Genes: 155 | TaxMap | GenBank FTP | Seq.S |
| GC Content: 38% | Others: 153 | TaxPlot | BLAST | Seque |
| Topology: circular | Total: 466 | GenePlot | TraceAssembly | Comp |
| Molecule: DNA | Contigs: 1 | gMap | CDD | Organ |
| Gen.Code: 1 | | | | Other genomes for species |

Gene Classification based on [COG functional categories](#)

Search gene, GeneID or locus_tag:

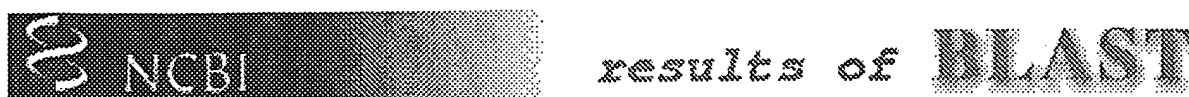


Comment and suggestions to: [\[info@ncbi.nlm.nih.gov\]](mailto:info@ncbi.nlm.nih.gov)

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[Department of Health & Human Services](#)
[Privacy Statement](#) | [Freedom of Information Act](#) | [Disclaimer](#)

Feb 6 2006 06:28:59

**BLASTN 2.2.13 [Nov-27-2005]****Reference:**

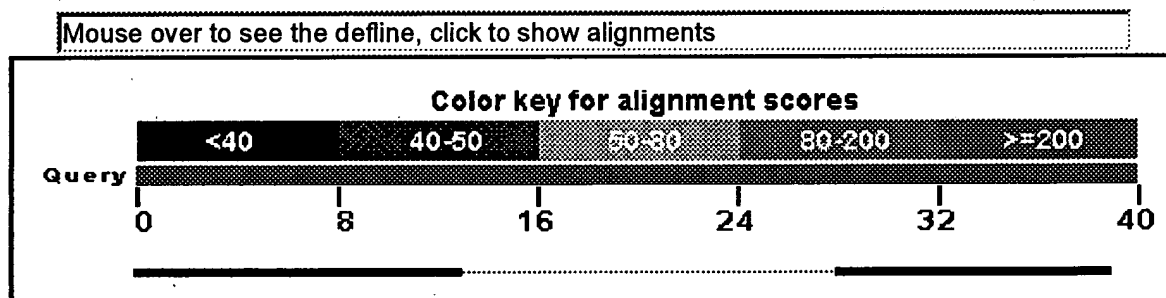
Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1139520074-12515-142933253334.BLASTQ4

Database: NCBI Genomic Reference Sequences
648,380 sequences; 5,833,944,919 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)
[Taxonomy reports](#)

Query=
Length=40

Distribution of 3 Blast Hits on the Query Sequence

| Sequences producing significant alignments: | Score (Bits) | E Value |
|--|-----------------|------------|
| gi 11994090 ref NC_001666.2 Zea mays chloroplast, complete geno | 22.3 | 0.80 |

Alignments[Get selected sequences](#)[Select all](#)[Deselect all](#)

> ☐ [gi|11994090|ref|NC_001666.2|](#) ☒ Zea mays chloroplast, complete genome
Length=140384

Score = 22.3 bits (11), Expect = 0.80
Identities = 11/11 (100%), Gaps = 0/11 (0%)
Strand=Plus/Plus

Query 3 TCGATCCAAA 13
 |||||
 Sbjct 66973 TCGATCCAAA 66983

Score = 22.3 bits (11), Expect = 0.80
 Identities = 11/11 (100%), Gaps = 0/11 (0%)
 Strand=Plus/Plus

Query 1 AATCGATCCAA 11
 |||||
 Sbjct 73754 AATCGATCCAA 73764

Score = 22.3 bits (11), Expect = 0.80
 Identities = 11/11 (100%), Gaps = 0/11 (0%)
 Strand=Plus/Plus

Query 29 TGGAAGAAAGA 39
 |||||
 Sbjct 112529 TGGAAGAAAGA 112539

Database: NCBI Genomic Reference Sequences

Posted date: Feb 7, 2006 12:38 PM

Number of letters in database: 142,297

Number of sequences in database: 2

Lambda K H
 1.37 0.711 1.31

Gapped
 Lambda K H
 1.37 0.711 1.31

Matrix: blastn matrix:1 -3

Gap Penalties: Existence: 5, Extension: 2

Number of Sequences: 2

Number of Hits to DB: 0

Number of extensions: 0

Number of successful extensions: 0

Number of sequences better than 10: 0

Number of HSP's better than 10 without gapping: 0

Number of HSP's gapped: 0

Number of HSP's successfully gapped: 0

Length of query: 40

Length of database: 142297

Length adjustment: 11

Effective length of query: 29

Effective length of database: 142297

Effective search space: 4126613

Effective search space used: 4125975

A: 0

X1: 10 (19.8 bits)

X2: 15 (29.7 bits)

X3: 25 (49.6 bits)

S1: 10 (20.3 bits)